VH DOMAIN

```
                    10                  20                  30                  40
MaE11       DVQLQESGPG      LVKPSQSLSL      ACSVTGYSITS      [GYSWN]WIRQF
            *   *   *         * **  *       * * *                          *
F(ab)-2     EVQLVESGGG      LVQPGGSLRL      SCAVSGYSITS      [GYSWN]WIRQA
                                              * ****           * ***   *
humIII      EVQLVESGGG      LVQPGGSLRL      SCAASGFTF-S      [DYAMS]WVRQA

                   49                  60                  70                  80
MaE11       PGNKLEWMG       [SITYDGSSNYN PSLKN]RISVT        RDTSQNQFFL
              **    **                *  *  * * *  ****       * * * * **
F(ab)-2     PGKGLEWVA       [SITYDGSTNYA DSVKG]RFTIS        RDDSKNTFYL
                             * ***** *
humIII      PGKGLEWVA       [VISNGSDTYYA DSVKG]RFTIS        RDDSKNTLYL

            82abc       90          100abcd   103           113
MaE11       KLNSATAEDTATY   YCAR[GSHYFGHWHFAV]   WGAGTTVT    VSS
            **  **      *                 *  *
F(ab)-2     QMNSLRAEDTAVY   YCAR[GSHYFGHWHFAV]   WGQGTLVT    VSS
                              * ** ******
humIII      QMNSLRAEDTAVY   YCAR[DSRFF-----DV]   WGQGTLVT    VSS
```

VL DOMAIN

```
                    10                  20                  30 32abcd       40
MaE11       DIQLTQSPAS      LAVSLGQRAT      ISC[KASQSVD YDGDSYMN]WYQQKP
                    *         ** * * *        *  *
F(ab)-2     DIQLTQSPSS      LSASVGDRVT      ITC[RASQSVD YDGDSYMN]WYQQKP
                                                    ****  *
humk1       DIQMTQSPSS      LSASVGDRVT      ITC[RASQSVD IS--SYLN]WYQQKP

                   49                  60                  70                  80
MaE11       GQPPILLIY       [AASYLGS]EIPA RFSGSGSGTD        FTLNIHPVEE
              ** *                    *  ** *                    * *****
F(ab)-2     GKAPKLLIY       [AASYLES]GVPS RFSGSGSGTD        FTLTISSLQP
                                    *
humkI       GKAPKLLIY       [AASSLES]GVPS RFSGSGSGTD        FTLTISSLQP

                   88                  97                 107
MaE11       EDAATFYC        [QQSHEDPYT]     FGAGTKLEIK
              *  *                             *   *
F(ab)-2     EDFATYYC        [QQSHEDPYT]     FGQGTKVEIK
                             ****
humk1       EDFATYYC        [QQYNSLPYT]     FGQGTKVEIK
```

FIG._1

LIGHT CHAIN

	10	20	30	40
e27	DIQLTQSPSS	LSASVGDRVT	ITCRASKPVD	GEGDSYLNWY
e26	DIQLTQSPSS	LSASVGDRVT	ITCRASKPVD	GEGDSYLNWY
e426	DIQLTQSPSS	LSASVGDRVT	ITCRASQSVD	YEGDSYLNWY
e25	DIQLTQSPSS	LSASVGDRVT	ITCRASQSVD	YDGDSYMNWY
				CDR-L1

	50	60	70	80
e27	QQKPGKAPKL	LIYAASYLES	GVPSRFSGSG	SGTDFTLTIS
e26	QQKPGKAPKL	LIYAASYLES	GVPSRFSGSG	SGTDFTLTIS
e426	QQKPGKAPKL	LIYAASYLES	GVPSRFSGSG	SGTDFTLTIS
e25	QQKPGKAPKL	LIYAASYLES	GVPSRFSGSG	SGTDFTLTIS
		CDR-L2		

	90	100	110	
e27	SLQPEDFATY	YCQQSHEDPY	TFGQGTKVEI	KRTV
e26	SLQPEDFATY	YCQQSHEDPY	TFGQGTKVEI	KRTV
e426	SLQPEDFATY	YCQQSHEDPY	TFGQGTKVEI	KRTV
e25	SLQPEDFATY	YCQQSHEDPY	TFGQGTKVEI	KRTV
		CDR-L3		

HEAVY CHAIN

	10	20	30	40
e27	EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ
e26	EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ
e426	EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ
e25	EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ
				CDR-H1

	50	60	70	80
e27	APGKGLEWVA	SIKYSGETKY	NPSVKGRITI	SRDDSKNTFY
e26	APGKGLEWVA	SITYDGSTNY	NPSVKGRITI	SRDDSKNTFY
e426	APGKGLEWVA	SITYDGSTNY	NPSVKGRITI	SRDDSKNTFY
e25	APGKGLEWVA	SITYDGSTNY	NPSVKGRITI	SRDDSKNTFY
		CDR-H2		

	90	100	110	
e27	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQG
e26	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQG
e426	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQG
e25	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQG
			CDR-H3	

FIG._2

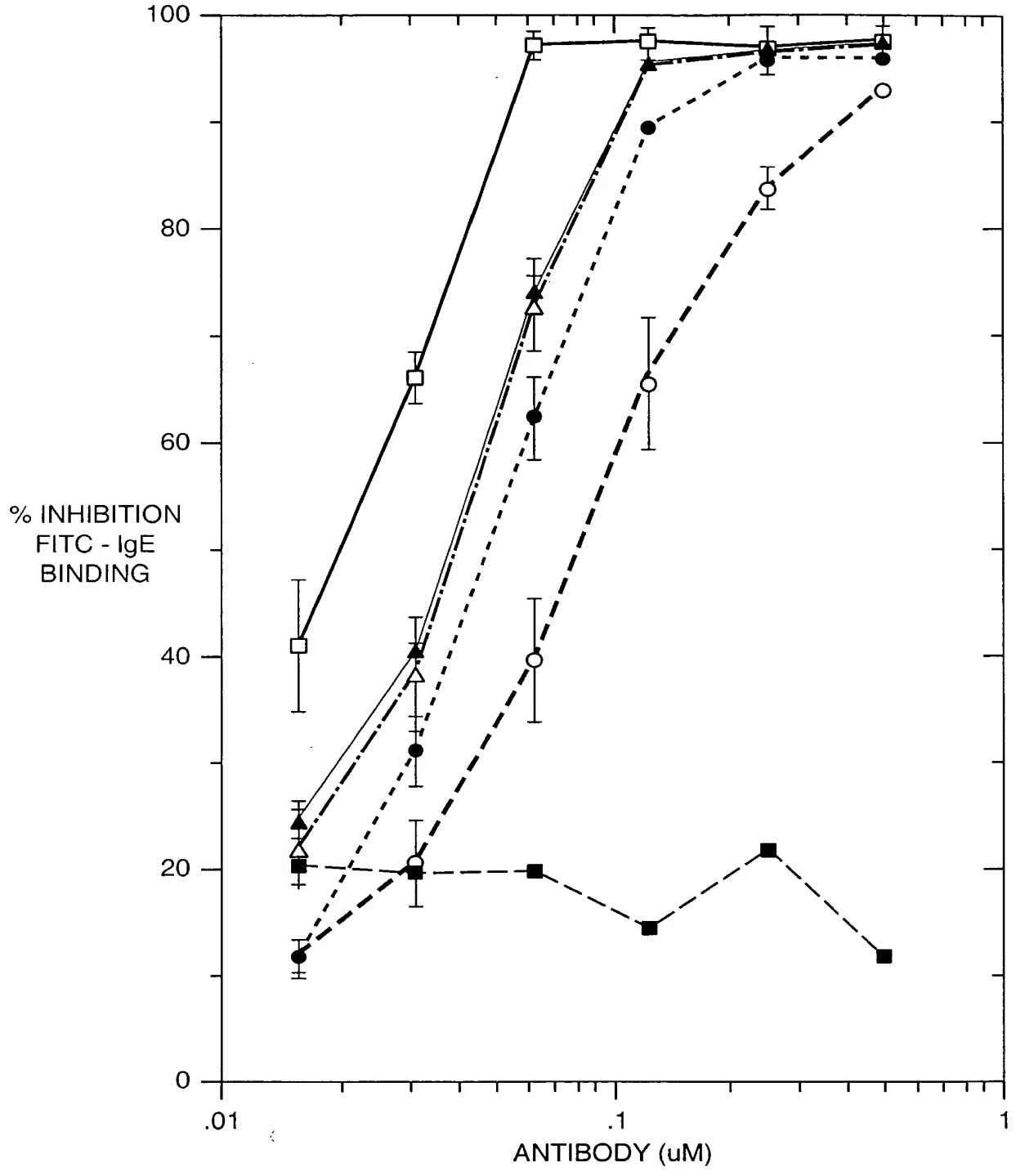


FIG._3

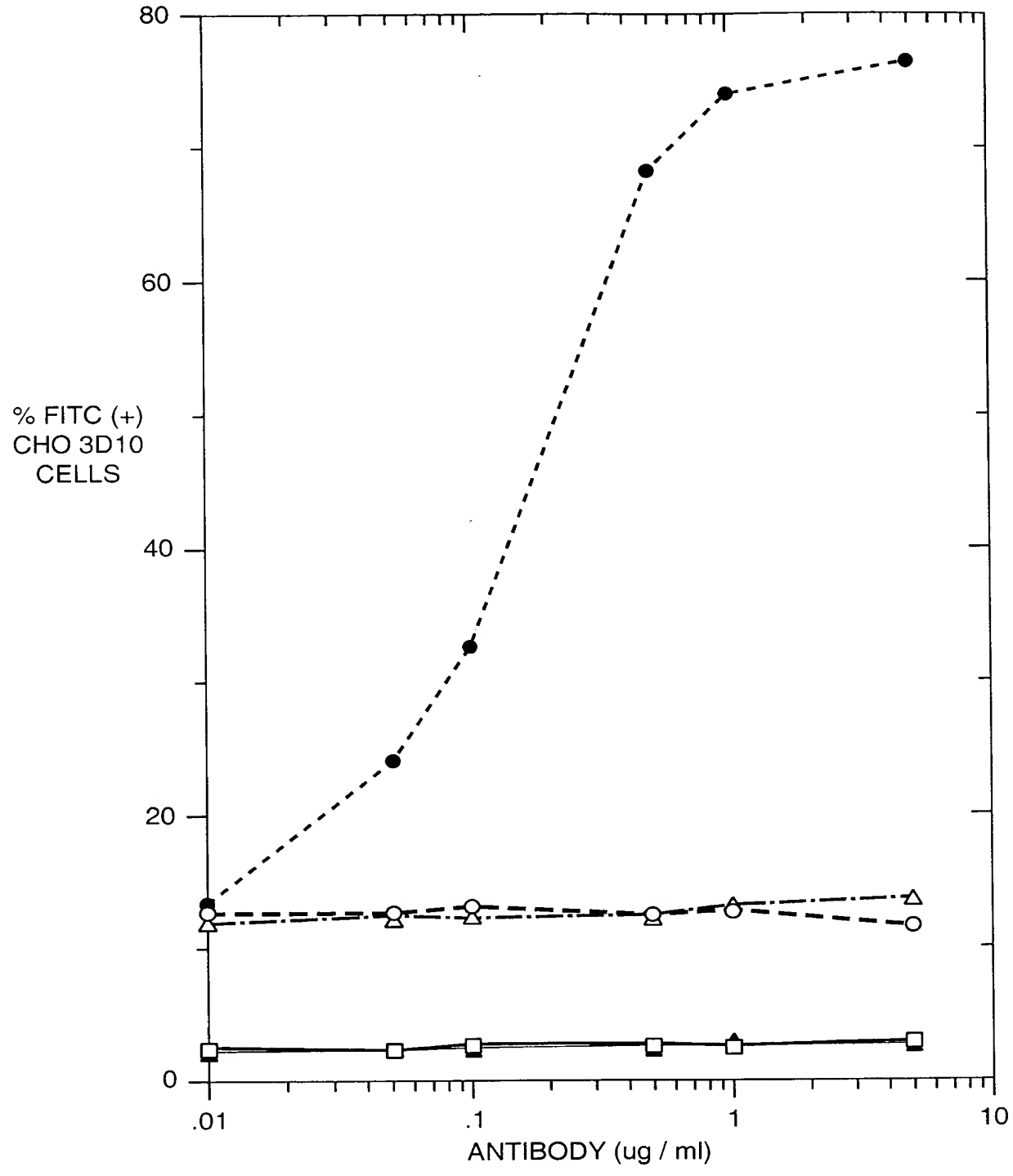
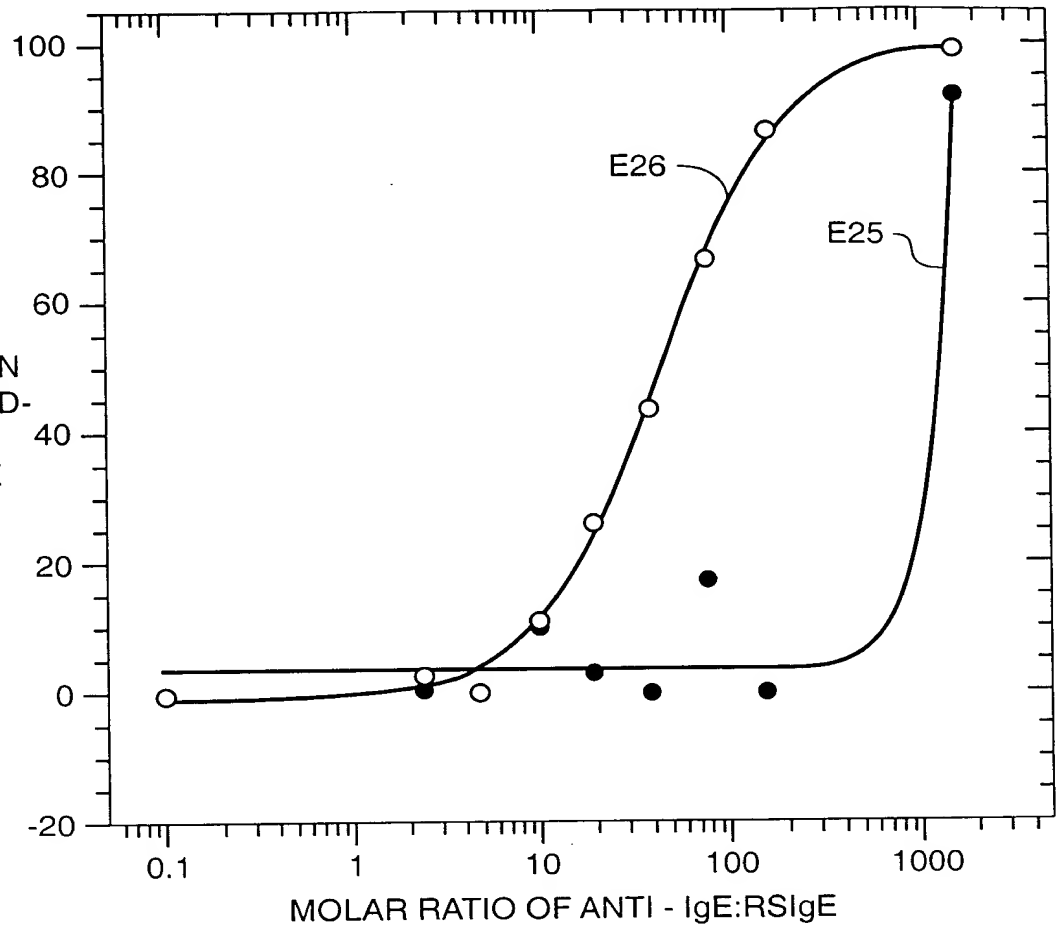


FIG._4



y = ((m1 - m4) / (1 + (m0 / m3)^m2))...		
	VALUE	ERROR
m1	3.7289	3.2575
m2	3.2312	2044.6
m3	3421.3	7.095e+07
m4	1226.5	7.4139e+07
Chisq	293.26	NA
R	0.97929	NA

y = ((m1 - m4) / (1 + (m0 / m3)^m2))...		
	VALUE	ERROR
m1	-0.78645	1.7681
m2	1.3544	0.11267
m3	44.486	3.1931
m4	100.07	2.6239
Chisq	31.442	NA
R	0.99867	NA

FIG._5

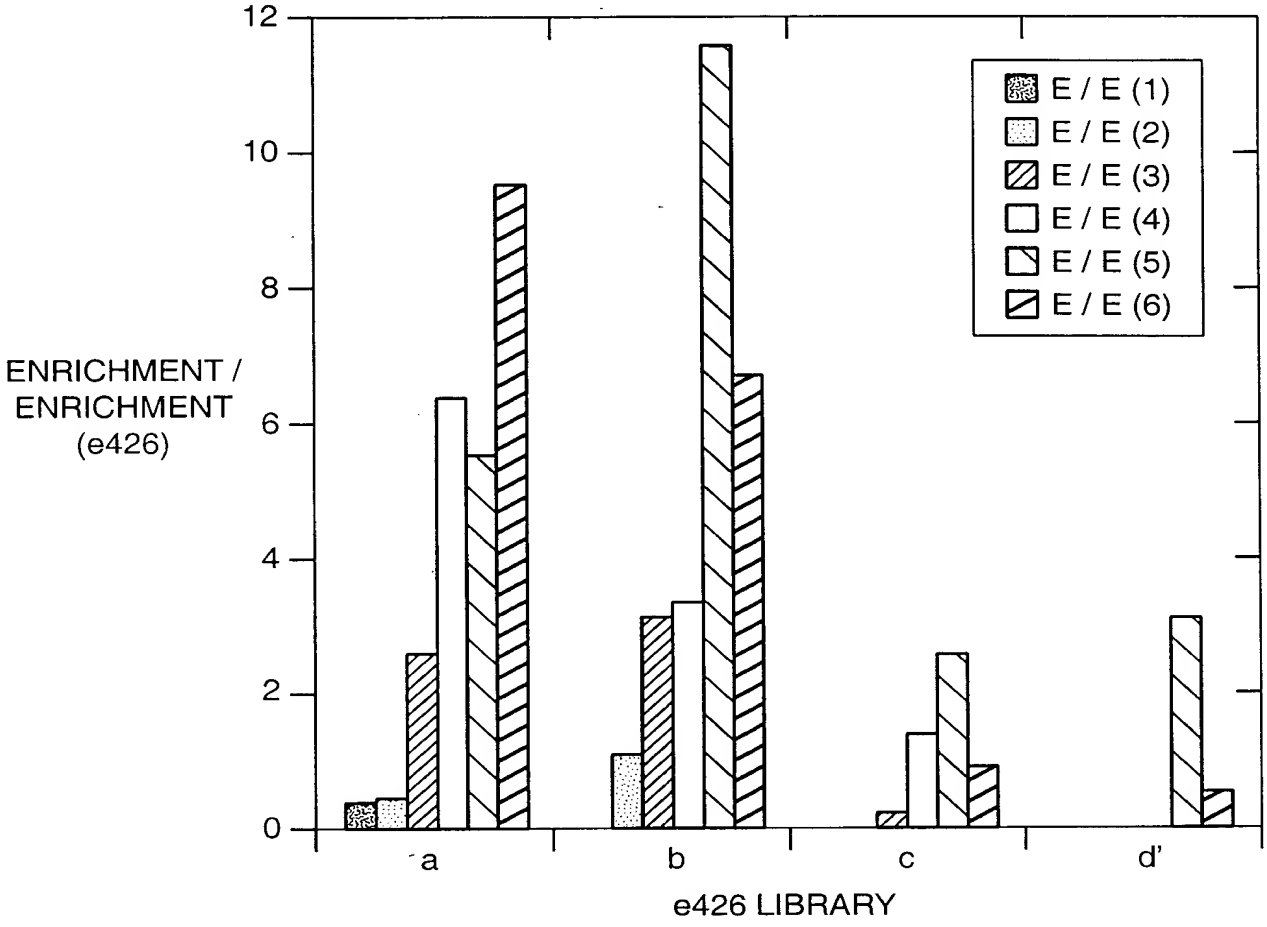


FIG._6

APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

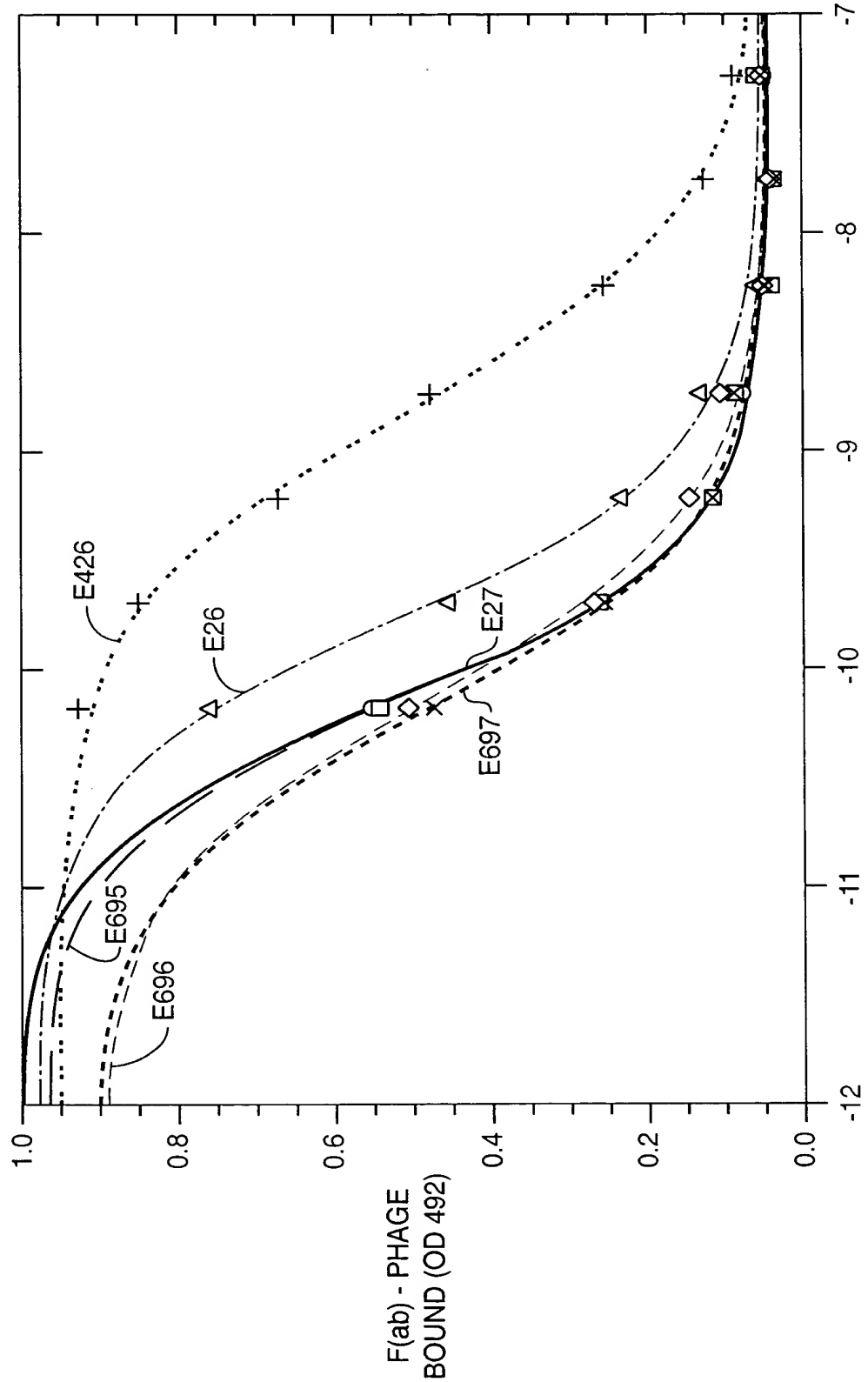


FIG._7

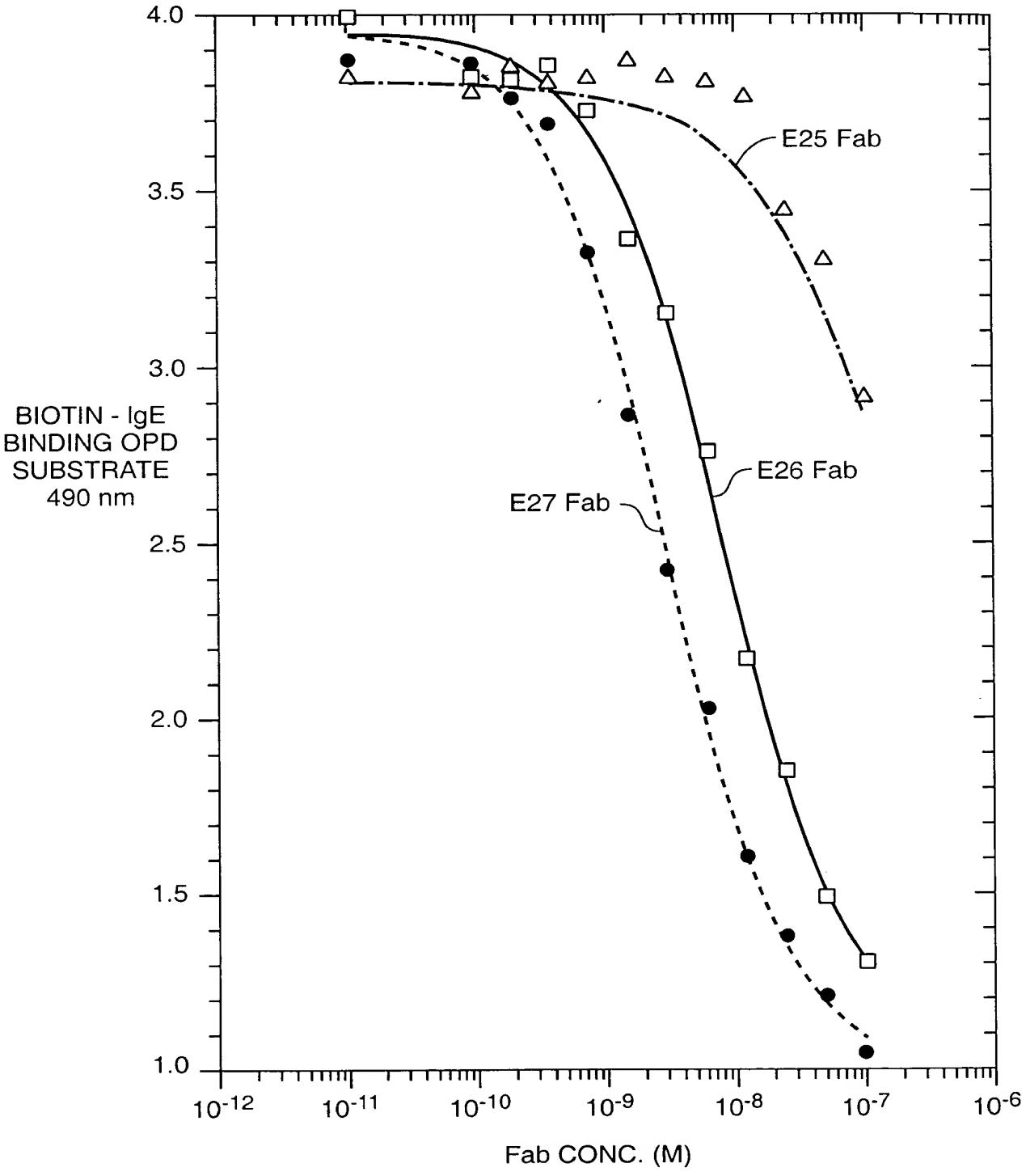


FIG._8

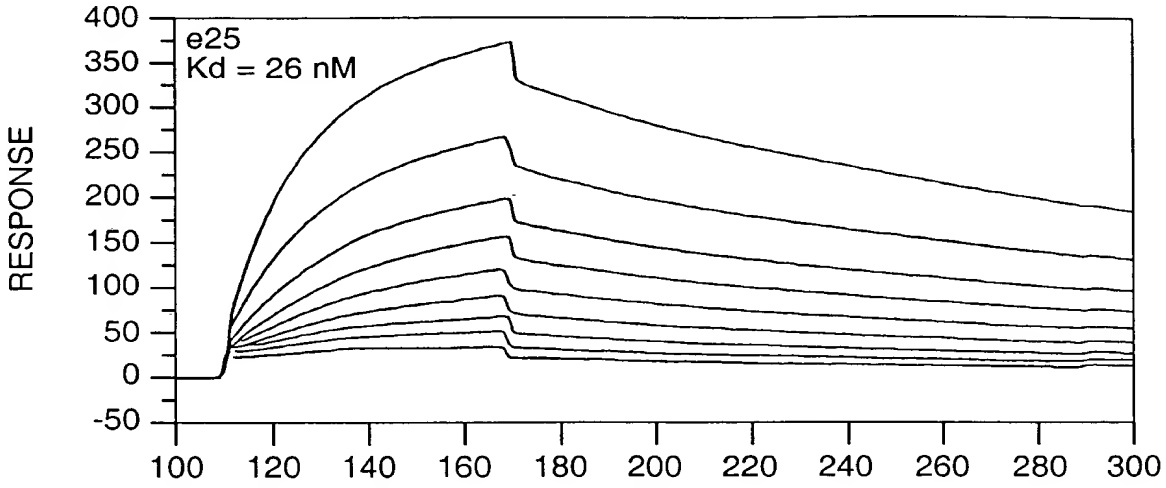


FIG._9A

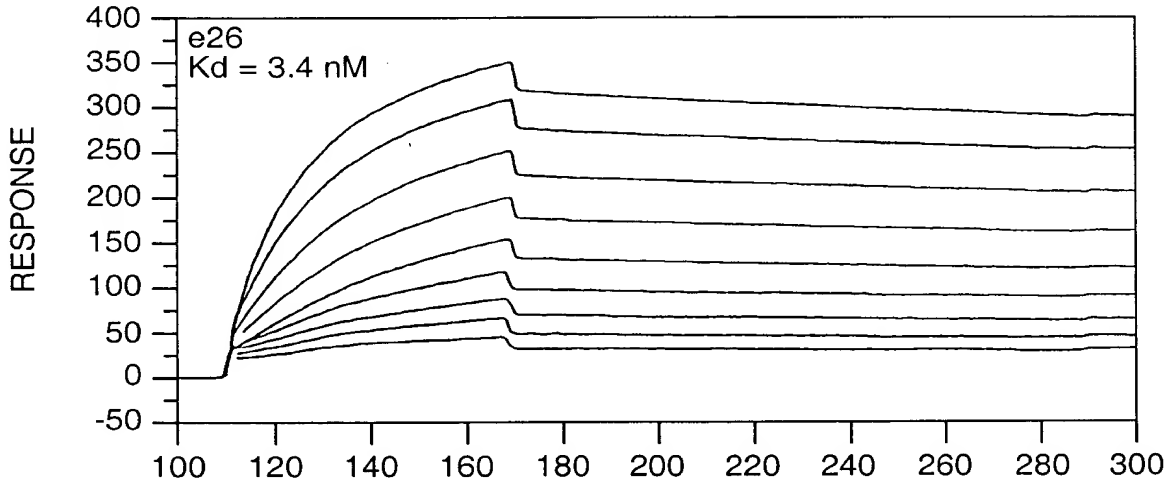


FIG._9B

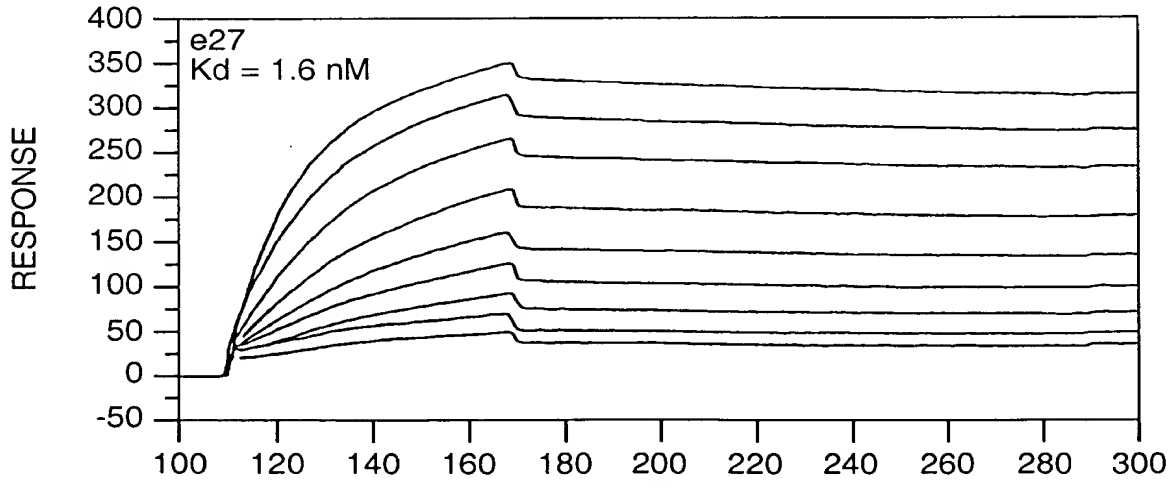


FIG._9C

```
  1  GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
     CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTTCTTCT TCTCAGCTTA

101  GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
     CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

201  GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
     CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301  AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GAATTCGAGC
     TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CTTAAGCTCG

401  TCGGTACCCG GGGATCCTCT CGAGGTTGAG GTGATTTTAT GAAAAAGAAT ATCGCATTTC TTCTTGCATC TATGTTCGTT TTTTCTATTG CTACAAACGC
     AGCCATGGGC CCCTAGGAGA GCTCCAACTC CACTAAAATA CTTTTTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA AAAAGATAAC GATGTTTGCG

501  GTACGCTGAT ATCCAGCTGA CCCAGTCCCC GAGCTCCCTG TCCGCCTCTG TGGGCGATAG GGTCACCATC ACCTGCCGTG CCAGTCAGAG CGTCGATTAC
     CATGCGACTA TAGGTCGACT GGGTCAGGGG CTCGAGGGAC AGGCGGAGAC ACCCGCTATC CCAGTGGTAG TGGACGGCAC GGTCAGTCTC GCAGCTAATG
  1      AlaAsp IleGlnLeuT hrGlnSerPr oSerSerLeu SerAlaSerV alGlyAspAr gValThrIle ThrCysArgA laSerGlnSe rValAspTyr
         Begin light chain

601  GAAGGTGATA GCTACCTGAA CTGGTATCAA CAGAAACCAG GAAAAGCTCC GAAACTACTG ATTTACGCGG CCTCGTACCT GGAGTCTGGA GTCCCTTCTC
     CTTCCACTAT CGATGGACTT GACCATAGTT GTCTTTGGTC CTTTTCGAGG CTTTGATGAC TAAATGCGCC GGAGCATGGA CCTCAGACCT CAGGGAAGAG
 33  GluGlyAspS erTyrLeuAs nTrpTyrGln GlnLysProG lyLysAlaPr oLysLeuLeu IleTyrAlaA laSerTyrLe uGluSerGly ValProSerArg

701  GCTTCTCTGG ATCCGGTTCT GGGACGGATT TCACTCTGAC CATCAGCAGT CTGCAGCCAG AAGACTTCGC AACTTATTAC TGTCAGCAAA GTCACGAGGA
     CGAAGAGACC TAGGCCAAGA CCCTGCCTAA AGTGAGACTG GTAGTCGTCA GACGTCGGTC TTCTGAAGCG TTGAATAATG ACAGTCGTTT CAGTGCTCCT
 67    PheSerGl ySerGlySer GlyThrAspP heThrLeuTh rIleSerSer LeuGlnProG luAspPheAl aThrTyrTyr CysGlnGlnS erHisGluAsp

801  TCCGTACACA TTTGGACAGG GTACCAAGGT GGAGATCAAA CGAACTGTGG CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT
     AGGCATGTGT AAACCTGTCC CATGGTTCCA CCTCTAGTTT GCTTGACACC GACGTGGTAG ACAGAAGTAG AAGGGCGGTA GACTACTCGT CAACTTTAGA
100   ProTyrThr PheGlyGlnG lyThrLysVa lGluIleLys ArgThrValA laAlaProSe rValPheIle PheProProS erAspGluGl nLeuLysSer

901  GGAACTGCTT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG
     CCTTGACGAA GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG GTTTCATGTC ACCTTCCACC TATTGCGGGA GGTTAGCCCA TTGAGGGTCC
133  GlyThrAlaS erValValCy sLeuLeuAsn AsnPheTyrP roArgGluAl aLysValGln TrpLysValA spAsnAlaLe uGlnSerGly AsnSerGlnGlu
```

FIG._10A

```
1001  AGAGTGTCAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG
      TCTCACAGTG TCTCGTCCTG TCGTTCCTGT CGTGGATGTC GGAGTCGTCG TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCGGAC
 167    SerValTh rGluGlnAsp SerLysAspS erThrTyrSe rLeuSerSer ThrLeuThrL euSerLysAl aAspTyrGlu LysHisLysV alTyrAlaCys

1101  CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA GGGGAGAGTG TTAAGCTGAT CCTCTACGCC GGACGCATCG TGGCCCTAGT
      GCTTCAGTGG GTAGTCCCGG ACTCGAGCGG GCAGTGTTTC TCGAAGTTGT CCCCTCTCAC AATTCGACTA GGAGATGCGG CCTGCGTAGC ACCGGGATCA
 200   GluValThr HisGlnGlyL euSerSerPr oValThrLys SerPheAsnA rgGlyGluCy sOC*
                                                                end light chain

1201  ACGCAAGTTC ACGTAAAAAG GGTATCTAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA
      TGCGTTCAAG TGCATTTTTC CCATAGATCT CCAACTCCAC TAAAATACTT TTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA AGATAACGAT

1301  CAAACGCGTA CGCTGAGGTT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG CAGCCAGGGG GCTCACTCCG TTTGTCCTGT GCAGTTTCTG GCTACTCCAT
      GTTTGCGCAT GCGACTCCAA GTCGACCACC TCAGACCGCC ACCGGACCAC GTCGGTCCCC CGAGTGAGGC AAACAGGACA CGTCAAAGAC CGATGAGGTA
   1                GluVal GlnLeuValG luSerGlyGl yGlyLeuVal GlnProGlyG lySerLeuAr gLeuSerCys AlaValSerG lyTyrSerIle
                    Begin heavy chain

1401  CACCTCCGGA TACAGCTGGA ACTGGATCCG TCAGGCCCCG GGTAAGGGCC TGGAATGGGT TGCATCGATT ACGTATGACG GATCGACTAA CTATAACCCT
      GTGGAGGCCT ATGTCGACCT TGACCTAGGC AGTCCGGGGC CCATTCCCGG ACCTTACCCA ACGTAGCTAA TGCATACTGC CTAGCTGATT GATATTGGGA
  30   ThrSerGly TyrSerTrpA snTrpIleAr gGlnAlaPro GlyLysGlyL euGluTrpVa lAlaSerIle ThrTyrAspG lySerThrAs nTyrAsnPro

1501  AGCGTCAAGG GCCGTATCAC TATAAGTCGC GACGATTCCA AAAACACATT CTACCTGCAG ATGAACAGCC TGCGTGCTGA GGACACTGCC GTCTATTATT
      TCGCAGTTCC CGGCATAGTG ATATTCAGCG CTGCTAAGGT TTTTGTGTAA GATGGACGTC TACTTGTCGG ACGCACGACT CCTGTGACGG CAGATAATAA
  63  SerValLysG lyArgIleTh rIleSerArg AspAspSerL ysAsnThrPh eTyrLeuGln MetAsnSerL euArgAlaGl uAspThrAla ValTyrTyrCys

1601  GTGCTCGAGG CAGCCACTAT TTCGGTCACT GGCACTTCGC CGTGTGGGGT CAAGGAACCC TGGTCACCGT CTCCTCGGCC TCCACCAAGG GCCCATCGGT
      CACGAGCTCC GTCGGTGATA AAGCCAGTGA CCGTGAAGCG GCACACCCCA GTTCCTTGGG ACCAGTGGCA GAGGAGCCGG AGGTGGTTCC CGGGTAGCCA
  97    AlaArgGl ySerHisTyr PheGlyHisT rpHisPheAl aValTrpGly GlnGlyThrL euValThrVa lSerSerAla SerThrLysG lyProSerVal

1701  CTTCCCCCTA GCACCCTCCT CCAAGAGCAC CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG
      GAAGGGGGAT CGTGGGAGGA GGTTCTCGTG GAGACCCCCG TGTCGCCGGG ACCCGACGGA CCAGTTCCTG ATGAAGGGGC TTGGCCACTG CCACAGCACC
 130   PheProLeu AlaProSerS erLysSerTh rSerGlyGly ThrAlaAlaL euGlyCysLe uValLysAsp TyrPheProG luProValTh rValSerTrp

1801  AACTCAGGCG CCCTGACCAG CGGCGTGCAC ACCTTCCCGG CTGTCCTACA GTCCTCAGGA CTCTACTCCC TCAGCAGCGT GGTGACCGTG CCCTCCAGCA
      TTGAGTCCGC GGGACTGGTC GCCGCACGTG TGGAAGGGCC GACAGGATGT CAGGAGTCCT GAGATGAGGG AGTCGTCGCA CCACTGGCAC GGGAGGTCGT
 163  AsnSerGlyA laLeuThrSe rGlyValHis ThrPheProA laValLeuGl nSerSerGly LeuTyrSerL euSerServa lValThrVal ProSerSerSer
```

FIG._10B

```
1901  GCTTGGGCAC CCAGACCTAC ATCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGAAAGT TGAGCCCAAA TCTTGTGACA AAACTCACAC
      CGAACCCGTG GGTCTGGATG TAGACGTTGC ACTTAGTGTT CGGGTCGTTG TGGTTCCACC TGTTCTTTCA ACTCGGGTTT AGAACACTGT TTTGAGTGTG
 197    LeuGlyTh rGlnThrTyr IleCysAsnV alAsnHisLy sProSerAsn ThrLysValA spLysLysVa lGluProLys SerCysAspL ysThrHisThr
                                                                                                 end of heavy chain

2001  CTAGAGTGGC GGTGGCTCTG GTTCCGGTGA TTTTGATTAT GAAAAGATGG CAAACGCTAA TAAGGGGGCT ATGACCGAAA ATGCCGATGA AAACGCGCTA
      GATCTCACCG CCACCGAGAC CAAGGCCACT AAAACTAATA CTTTTCTACC GTTTGCGATT ATTCCCCCGA TACTGGCTTT TACGGCTACT TTTGCGCGAT
 230   AM*SerGly GlyGlySerG lySerGlyAs pPheAspTyr GluLysMetA laAsnAlaAs nLysGlyAla MetThrGluA snAlaAspGl uAsnAlaLeu
       fusion to g3p C-terminal domain

2101  CAGTCTGACG CTAAAGGCAA ACTTGATTCT GTCGCTACTG ATTACGGTGC TGCTATCGAT GGTTTCATTG GTGACGTTTC CGGCCTTGCT AATGGTAATG
      GTCAGACTGC GATTTCCGTT TGAACTAAGA CAGCGATGAC TAATGCCACG ACGATAGCTA CCAAAGTAAC CACTGCAAAG GCCGGAACGA TTACCATTAC
 263  GlnSerAspA laLysGlyLy sLeuAspSer ValAlaThrA spTyrGlyAl aAlaIleAsp GlyPheIleG lyAspValSe rGlyLeuAla AsnGlyAsnGly

2201  GTGCTACTGG TGATTTTGCT GGCTCTAATT CCCAAATGGC TCAAGTCGGT GACGGTGATA ATTCACCTTT AATGAATAAT TTCCGTCAAT ATTTACCTTC
      CACGATGACC ACTAAAACGA CCGAGATTAA GGGTTTACCG AGTTCAGCCA CTGCCACTAT TAAGTGGAAA TTACTTATTA AAGGCAGTTA TAAATGGAAG
 297    AlaThrGl yAspPheAla GlySerAsnS erGlnMetAl aGlnValGly AspGlyAspA snSerProLe uMetAsnAsn PheArgGlnT yrLeuProSer

2301  CCTCCCTCAA TCGGTTGAAT GTCGCCCTTT TGTCTTTAGC GCTGGTAAAC CATATGAATT TTCTATTGAT TGTGACAAAA TAAACTTATT CCGTGGTGTC
      GGAGGGAGTT AGCCAACTTA CAGCGGGAAA ACAGAAATCG CGACCATTTG GTATACTTAA AAGATAACTA ACACTGTTTT ATTTGAATAA GGCACCACAG
 330   LeuProGln SerValGluC ysArgProPh eValPheSer AlaGlyLysP roTyrGluPh eSerIleAsp CysAspLysI leAsnLeuPh eArgGlyVal

2401  TTTGCGTTTC TTTTATATGT TGCCACCTTT ATGTATGTAT TTTCTACGTT TGCTAACATA CTGCGTAATA AGGAGTCTTA ATCATGCCAG TTCTTTTGGC
      AAACGCAAAG AAAATATACA ACGGTGGAAA TACATACATA AAAGATGCAA ACGATTGTAT GACGCATTAT TCCTCAGAAT TAGTACGGTC AAGAAAACCG
 363  PheAlaPheL euLeuTyrVa lAlaThrPhe MetTyrValP heSerThrPh eAlaAsnIle LeuArgAsnL ysGluSerOC *
                                                                          end of g3p domain

2501  TAGCGCCGCC CTATACCTTG TCTGCCTCCC CGCGTTGCGT CGCGGTGCAT GGAGCCGGGC CACCTCGACC TGAATGGAAG CCGGCGGCAC CTCGCTAACG
      ATCGCGGCGG GATATGGAAC AGACGGAGGG GCGCAACGCA GCGCCACGTA CCTCGGCCCG GTGGAGCTGG ACTTACCTTC GGCCGCCGTG GAGCGATTGC

2601  GATTCACCAC TCCAAGAATT GGAGCCAATC AATTCTTGCG GAGAACTGTG AATGCGCAAA CCAACCCTTG GCAGAACATA TCCATCGCGT CCGCCATCTC
      CTAAGTGGTG AGGTTCTTAA CCTCGGTTAG TTAAGAACGC CTCTTGACAC TTACGCGTTT GGTTGGGAAC CGTCTTGTAT AGGTAGCGCA GGCGGTAGAG

2701  CAGCAGCCGC ACGCGGCGCA TCTCGGGCAG CGTTGGGTCC TGGCCACGGG TGCGCATGAT CGTGCTCCTG TCGTTGAGGA CCCGGCTAGG CTGGCGGGGT
      GTCGTCGGCG TGCGCCGCGT AGAGCCCGTC GCAACCCAGG ACCGGTGCCC ACGCGTACTA GCACGAGGAC AGCAACTCCT GGGCCGATCC GACCGCCCCA
```


FIG._10C

```
2801  TGCCTTACTG GTTAGCAGAA TGAATCACCG ATACGCGAGC GAACGTGAAG CGACTGCTGC TGCAAAACGT CTGCGACCTG AGCAACAACA TGAATGGTCT
      ACGGAATGAC CAATCGTCTT ACTTAGTGGC TATGCGCTCG CTTGCACTTC GCTGACGACG ACGTTTTGCA GACGCTGGAC TCGTTGTTGT ACTTACCAGA

2901  TCGGTTTCCG TGTTTCGTAA AGTCTGGAAA CGCGGAAGTC AGCGCCCTGC ACCATTATGT TCCGGATCTG CATCGCAGGA TGCTGCTGGC TACCCTGTGG
      AGCCAAAGGC ACAAAGCATT TCAGACCTTT GCGCCTTCAG TCGCGGGACG TGGTAATACA AGGCCTAGAC GTAGCGTCCT ACGACGACCG ATGGGACACC

3001  AACACCTACA TCTGTATTAA CGAAGCGCTG GCATTGACCC TGAGTGATTT TTCTCTGGTC CCGCCGCATC CATACCGCCA GTTGTTTACC CTCACAACGT
      TTGTGGATGT AGACATAATT GCTTCGCGAC CGTAACTGGG ACTCACTAAA AAGAGACCAG GGCGGCGTAG GTATGGCGGT CAACAAATGG GAGTGTTGCA

3101  TCCAGTAACC GGGCATGTTC ATCATCAGTA ACCCGTATCG TGAGCATCCT CTCTCGTTTC ATCGGTATCA TTACCCCCAT GAACAGAAAT TCCCCCTTAC
      AGGTCATTGG CCCGTACAAG TAGTAGTCAT TGGGCATAGC ACTCGTAGGA GAGAGCAAAG TAGCCATAGT AATGGGGGTA CTTGTCTTTA AGGGGGAATG

3201  ACGGAGGCAT CAAGTGACCA AACAGGAAAA AACCGCCCTT AACATGGCCC GCTTTATCAG AAGCCAGACA TTAACGCTTC TGGAGAAACT CAACGAGCTG
      TGCCTCCGTA GTTCACTGGT TTGTCCTTTT TTGGCGGGAA TTGTACCGGG CGAAATAGTC TTCGGTCTGT AATTGCGAAG ACCTCTTTGA GTTGCTCGAC

3301  GACGCGGATG AACAGGCAGA CATCTGTGAA TCGCTTCACG ACCACGCTGA TGAGCTTTAC CGCAGGATCC GGAAATTGTA AACGTTAATA TTTTGTTAAA
      CTGCGCCTAC TTGTCCGTCT GTAGACACTT AGCGAAGTGC TGGTGCGACT ACTCGAAATG GCGTCCTAGG CCTTTAACAT TTGCAATTAT AAAACAATTT

3401  ATTCGCGTTA AATTTTTGTT AAATCAGCTC ATTTTTTAAC CAATAGGCCG AAATCGGCAA AATCCCTTAT AAATCAAAAG AATAGACCGA GATAGGGTTG
      TAAGCGCAAT TTAAAAACAA TTTAGTCGAG TAAAAAATTG GTTATCCGGC TTTAGCCGTT TTAGGGAATA TTTAGTTTTC TTATCTGGCT CTATCCCAAC

3501  AGTGTTGTTC CAGTTTGGAA CAAGAGTCCA CTATTAAAGA ACGTGGACTC CAACGTCAAA GGGCGAAAAA CCGTCTATCA GGGCTATGGC CCACTACGTG
      TCACAACAAG GTCAAACCTT GTTCTCAGGT GATAATTTCT TGCACCTGAG GTTGCAGTTT CCCGCTTTTT GGCAGATAGT CCCGATACCG GGTGATGCAC

3601  AACCATCACC CTAATCAAGT TTTTTGGGGT CGAGGTGCCG TAAAGCACTA AATCGGAACC CTAAAGGGAG CCCCCGATTT AGAGCTTGAC GGGGAAAGCC
      TTGGTAGTGG GATTAGTTCA AAAAACCCCA GCTCCACGGC ATTTCGTGAT TTAGCCTTGG GATTTCCCTC GGGGGCTAAA TCTCGAACTG CCCCTTTCGG

3701  GGCGAACGTG GCGAGAAAGG AAGGGAAGAA AGCGAAAGGA GCGGGCGCTA GGGCGCTGGC AAGTGTAGCG GTCACGCTGC GCGTAACCAC CACACCCGCC
      CCGCTTGCAC CGCTCTTTCC TTCCCTTCTT TCGCTTTCCT CGCCCGCGAT CCCGCGACCG TTCACATCGC CAGTGCGACG CGCATTGGTG GTGTGGGCGG

3801  GCGCTTAATG CGCCGCTACA GGGCGCGTCC GGATCCTGCC TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA
      CGCGAATTAC GCGGCGATGT CCCGCGCAGG CCTAGGACGG AGCGCGCAAA GCCACTACTG CCACTTTTGG AGACTGTGTA CGTCGAGGGC CTCTGCCAGT

3901  CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG TTGGCGGGTG TCGGGGCGCA GCCATGACCC AGTCACGTAG
      GTCGAACAGA CATTCGCCTA CGGCCCTCGT CTGTTCGGGC AGTCCCGCGC AGTCGCCCAC AACCGCCCAC AGCCCCGCGT CGGTACTGGG TCAGTGCATC
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FIG._10D

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4001  CGATAGCGGA GTGTATACTG GCTTAACTAT GCGGCATCAG AGCAGATTGT ACTGAGAGTG CACCATATGC GGTGTGAAAT ACCGCACAGA TGCGTAAGGA
      GCTATCGCCT CACATATGAC CGAATTGATA CGCCGTAGTC TCGTCTAACA TGACTCTCAC GTGGTATACG CCACACTTTA TGGCGTGTCT ACGCATTCCT

4101  GAAAATACCG CATCAGGCGC TCTTCCGCTT CCTCGCTCAC TGACTCGCTG CGCTCGGTCG TTCGGCTGCG GCGAGCGGTA TCAGCTCACT CAAAGGCGGT
      CTTTTATGGC GTAGTCCGCG AGAAGGCGAA GGAGCGAGTG ACTGAGCGAC GCGAGCCAGC AAGCCGACGC CGCTCGCCAT AGTCGAGTGA GTTTCCGCCA

4201  AATACGGTTA TCCACAGAAT CAGGGGATAA CGCAGGAAAG AACATGTGAG CAAAAGGCCA GCAAAAGGCC AGGAACCGTA AAAAGGCCGC GTTGCTGGCG
      TTATGCCAAT AGGTGTCTTA GTCCCCTATT GCGTCCTTTC TTGTACACTC GTTTTCCGGT CGTTTTCCGG TCCTTGGCAT TTTTCCGGCG CAACGACCGC

4301  TTTTTCCATA GGCTCCGCCC CCCTGACGAG CATCACAAAA ATCGACGCTC AAGTCAGAGG TGGCGAAACC CGACAGGACT ATAAAGATAC CAGGCGTTTC
      AAAAAGGTAT CCGAGGCGGG GGGACTGCTC GTAGTGTTTT TAGCTGCGAG TTCAGTCTCC ACCGCTTTGG GCTGTCCTGA TATTTCTATG GTCCGCAAAG

4401  CCCCTGGAAG CTCCCTCGTG CGCTCTCCTG TTCCGACCCT GCCGCTTACC GGATACCTGT CCGCCTTTCT CCCTTCGGGA AGCGTGGCGC TTTCTCATAG
      GGGGACCTTC GAGGGAGCAC GCGAGAGGAC AAGGCTGGGA CGGCGAATGG CCTATGGACA GGCGGAAAGA GGGAAGCCCT TCGCACCGCG AAAGAGTATC

4501  CTCACGCTGT AGGTATCTCA GTTCGGTGTA GGTCGTTCGC TCCAAGCTGG GCTGTGTGCA CGAACCCCCC GTTCAGCCCG ACCGCTGCGC CTTATCCGGT
      GAGTGCGACA TCCATAGAGT CAAGCCACAT CCAGCAAGCG AGGTTCGACC CGACACACGT GCTTGGGGGG CAAGTCGGGC TGGCGACGCG GAATAGGCCA

4601  AACTATCGTC TTGAGTCCAA CCCGGTAAGA CACGACTTAT CGCCACTGGC AGCAGCCACT GGTAACAGGA TTAGCAGAGC GAGGTATGTA GGCGGTGCTA
      TTGATAGCAG AACTCAGGTT GGGCCATTCT GTGCTGAATA GCGGTGACCG TCGTCGGTGA CCATTGTCCT AATCGTCTCG CTCCATACAT CCGCCACGAT

4701  CAGAGTTCTT GAAGTGGTGG CCTAACTACG GCTACACTAG AAGGACAGTA TTTGGTATCT GCGCTCTGCT GAAGCCAGTT ACCTTCGGAA AAAGAGTTGG
      GTCTCAAGAA CTTCACCACC GGATTGATGC CGATGTGATC TTCCTGTCAT AAACCATAGA CGCGAGACGA CTTCGGTCAA TGGAAGCCTT TTTCTCAACC

4801  TAGCTCTTGA TCCGGCAAAC AAACCACCGC TGGTAGCGGT GGTTTTTTTG TTTGCAAGCA GCAGATTACG CGCAGAAAAA AAGGATCTCA AGAAGATCCT
      ATCGAGAACT AGGCCGTTTG TTTGGTGGCG ACCATCGCCA CCAAAAAAAC AAACGTTCGT CGTCTAATGC GCGTCTTTTT TTCCTAGAGT TCTTCTAGGA
4901  TTGATCTTTT CTACGGGGTC TGACGCTCAG TGGAACGAAA ACTCACGTTA AGGGATTTTG GTCATGAGAT TATCAAAAAG GATCTTCACC TAGATCCTTT
      AACTAGAAAA GATGCCCCAG ACTGCGAGTC ACCTTGCTTT TGAGTGCAAT TCCCTAAAAC CAGTACTCTA ATAGTTTTTC CTAGAAGTGG ATCTAGGAAA

5001  TAAATTAAAA ATGAAGTTTT AAATCAATCT AAAGTATATA TGAGTAAACT TGGTCTGACA GTTACCAATG CTTAATCAGT GAGGCACCTA TCTCAGCGAT
      ATTTAATTTT TACTTCAAAA TTTAGTTAGA TTTCATATAT ACTCATTTGA ACCAGACTGT CAATGGTTAC GAATTAGTCA CTCCGTGGAT AGAGTCGCTA

5101  CTGTCTATTT CGTTCATCCA TAGTTGCCTG ACTCCCCGTC GTGTAGATAA CTACGATACG GGAGGGCTTA CCATCTGGCC CCAGTGCTGC AATGATACCG
      GACAGATAAA GCAAGTAGGT ATCAACGGAC TGAGGGGCAG CACATCTATT GATGCTATGC CCTCCCGAAT GGTAGACCGG GGTCACGACG TTACTATGGC
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FIG._10E

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5201  CGAGACCCAC GCTCACCGGC TCCAGATTTA TCAGCAATAA ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA GTGGTCCTGC AACTTTATCC GCCTCCATCC
      GCTCTGGGTG CGAGTGGCCG AGGTCTAAAT AGTCGTTATT TGGTCGGTCG GCCTTCCCGG CTCGCGTCTT CACCAGGACG TTGAAATAGG CGGAGGTAGG

5301  AGTCTATTAA TTGTTGCCGG GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT AGTTTGCGCA ACGTTGTTGC CATTGCTGCA GGCATCGTGG TGTCACGCTC
      TCAGATAATT AACAACGGCC CTTCGATCTC ATTCATCAAG CGGTCAATTA TCAAACGCGT TGCAACAACG GTAACGACGT CCGTAGCACC ACAGTGCGAG

5401  GTCGTTTGGT ATGGCTTCAT TCAGCTCCGG TTCCCAACGA TCAAGGCGAG TTACATGATC CCCCATGTTG TGCAAAAAAG CGGTTAGCTC CTTCGGTCCT
      CAGCAAACCA TACCGAAGTA AGTCGAGGCC AAGGGTTGCT AGTTCCGCTC AATGTACTAG GGGGTACAAC ACGTTTTTTC GCCAATCGAG GAAGCCAGGA

5501  CCGATCGTTG TCAGAAGTAA GTTGGCCGCA GTGTTATCAC TCATGGTTAT GGCAGCACTG CATAATTCTC TTACTGTCAT GCCATCCGTA AGATGCTTTT
      GGCTAGCAAC AGTCTTCATT CAACCGGCGT CACAATAGTG AGTACCAATA CCGTCGTGAC GTATTAAGAG AATGACAGTA CGGTAGGCAT TCTACGAAAA

5601  CTGTGACTGG TGAGTACTCA ACCAAGTCAT TCTGAGAATA GTGTATGCGG CGACCGAGTT GCTCTTGCCC GGCGTCAACA CGGGATAATA CCGCGCCACA
      GACACTGACC ACTCATGAGT TGGTTCAGTA AGACTCTTAT CACATACGCC GCTGGCTCAA CGAGAACGGG CCGCAGTTGT GCCCTATTAT GGCGCGGTGT

5701  TAGCAGAACT TTAAAAGTGC TCATCATTGG AAAACGTTCT TCGGGGCGAA AACTCTCAAG GATCTTACCG CTGTTGAGAT CCAGTTCGAT GTAACCCACT
      ATCGTCTTGA AATTTTCACG AGTAGTAACC TTTTGCAAGA AGCCCCGCTT TTGAGAGTTC CTAGAATGGC GACAACTCTA GGTCAAGCTA CATTGGGTGA

5801  CGTGCACCCA ACTGATCTTC AGCATCTTTT ACTTTCACCA GCGTTTCTGG GTGAGCAAAA ACAGGAAGGC AAAATGCCGC AAAAAAGGGA ATAAGGGCGA
      GCACGTGGGT TGACTAGAAG TCGTAGAAAA TGAAAGTGGT CGCAAAGACC CACTCGTTTT TGTCCTTCCG TTTTACGGCG TTTTTTCCCT TATTCCCGCT

5901  CACGGAAATG TTGAATACTC ATACTCTTCC TTTTTCAATA TTATTGAAGC ATTTATCAGG GTTATTGTCT CATGAGCGGA TACATATTTG AATGTATTTA
      GTGCCTTTAC AACTTATGAG TATGAGAAGG AAAAAGTTAT AATAACTTCG TAAATAGTCC CAATAACAGA GTACTCGCCT ATGTATAAAC TTACATAAAT

6001  GAAAAATAAA CAAATAGGGG TTCCGCGCAC ATTTCCCCGA AAAGTGCCAC CTGACGTCTA AGAAACCATT ATTATCATGA CATTAACCTA TAAAAATAGG
      CTTTTTATTT GTTTATCCCC AAGGCGCGTG TAAAGGGGCT TTTCACGGTG GACTGCAGAT TCTTTGGTAA TAATAGTACT GTAATTGGAT ATTTTTATCC

6101  CGTATCACGA GGCCCTTTCG TCTTCAA
      GCATAGTGCT CCGGGAAAGC AGAAGTT
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FIG._10F

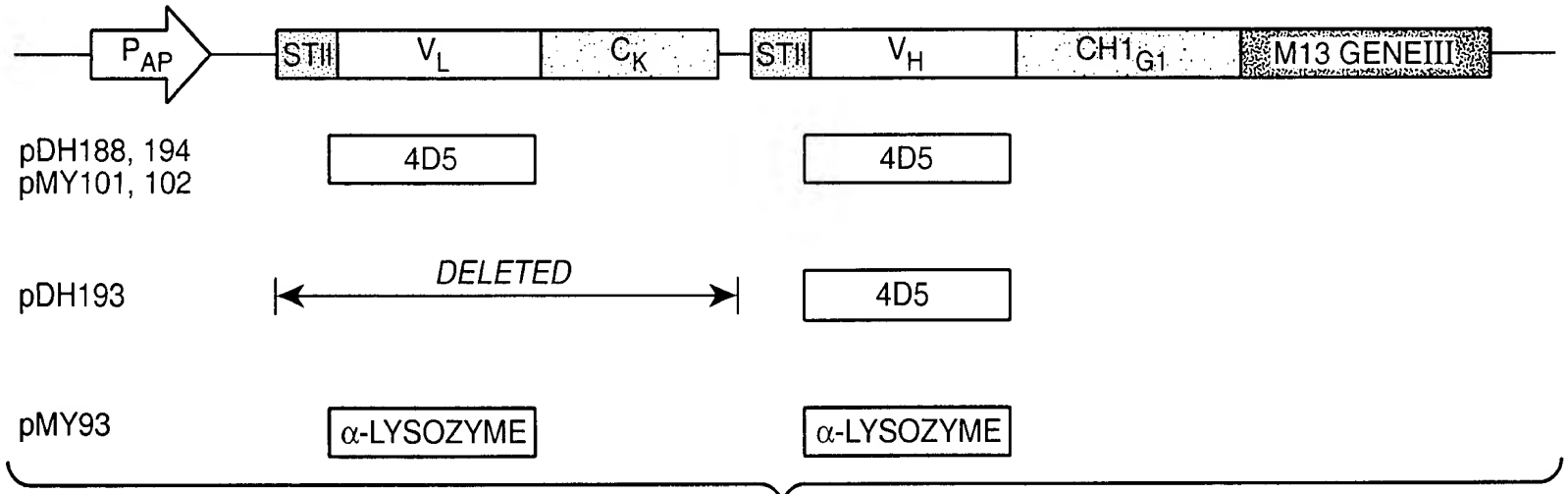

FIG._11A

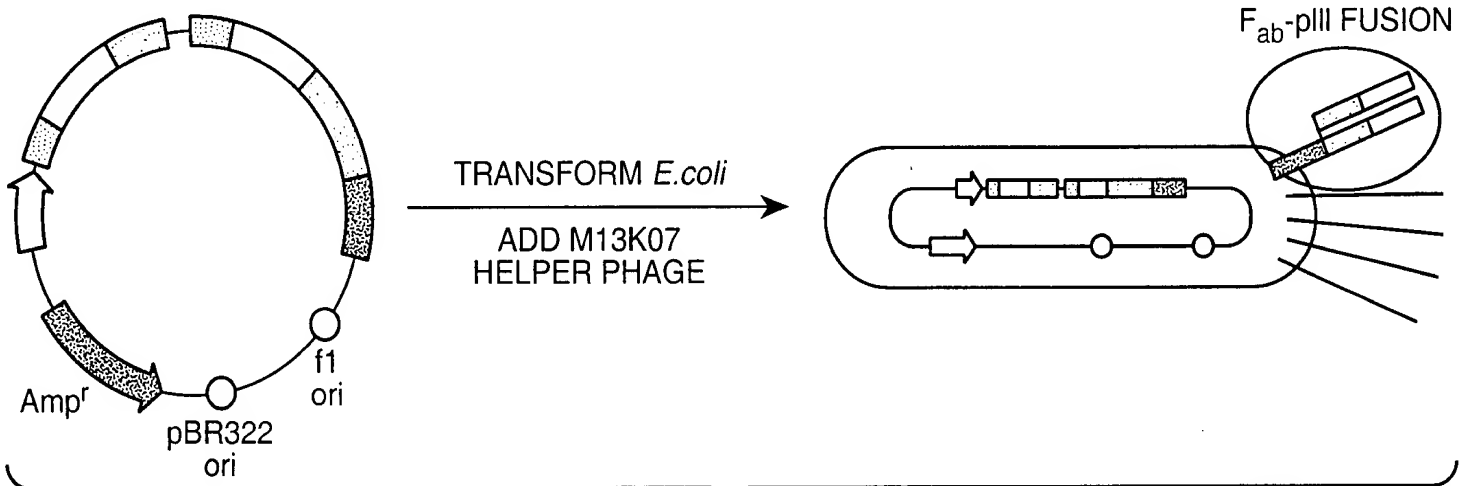

FIG._11B

(E25) - LIGHT CHAIN

DIQLTQSPSS LSASVGDRVT ITCRASQSVD YDGDSYMNWY QQKPGKAPKL LIYAASYLES GVPSRFSGSG
SGTDFTLTIS SLQPEDFATY YCQQSHEDPY TFGQGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL
NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV THQGLSSPVT
KSFNRGEC

(E25) - HEAVY CHAIN

EVQLVESGGG LVQPGGSLRL SCAVSGYSIT SGYSWNWIRQ APGKGLEWVA SITYDGSTNY NPSVKGRITI
SRDDSKNTFY LQMNSLRAED TAVYYCARGS HYFGHWHFAV WGQGTLVTVS SASTKGPSVF PLAPSSKSTS
GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP
SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN
WYVDGVEVHN AKTKPREEQY NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL YSKLTVDKSR
WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K

(E26) - LIGHT CHAIN

DIQLTQSPSS LSASVGDRVT ITCRASKPVD GEGDSYLNWY QQKPGKAPKL LIYAASYLES GVPSRFSGSG
SGTDFTLTIS SLQPEDFATY YCQQSHEDPY TFGQGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL
NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV THQGLSSPVT
KSFNRGEC

(E26) - HEAVY CHAIN

EVQLVESGGG LVQPGGSLRL SCAVSGYSIT SGYSWNWIRQ APGKGLEWVA SITYDGSTNY NPSVKGRITI
SRDDSKNTFY LQMNSLRAED TAVYYCARGS HYFGHWHFAV WGQGTLVTVS SASTKGPSVF PLAPSSKSTS
GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP
SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN
WYVDGVEVHN AKTKPREEQY NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL YSKLTVDKSR
WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K

(E27) - LIGHT CHAIN

DIQLTQSPSS LSASVGDRVT ITCRASKPVD GEGDSYLNWY QQKPGKAPKL LIYAASYLES GVPSRFSGSG
SGTDFTLTIS SLQPEDFATY YCQQSHEDPY TFGQGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL
NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV THQGLSSPVT
KSFNRGEC

(E27) - HEAVY CHAIN

EVQLVESGGG LVQPGGSLRL SCAVSGYSIT SGYSWNWIRQ APGKGLEWVA SIKYSGETKY NPSVKGRITI
SRDDSKNTFY LQMNSLRAED TAVYYCARGS HYFGHWHFAV WGQGTLVTVS SASTKGPSVF PLAPSSKSTS
GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP
SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN
WYVDGVEVHN AKTKPREEQY NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL YSKLTVDKSR
WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K

FIG._12

LIGHT CHAIN

E26

DIQLTQSPSS LSASVGDRVT ITCRASKPVD GEGDSYLNWY QQKPGKAPKL LIYAASYLES
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSHEDPY TFGQGTKVEI KRTVAAPSVF
IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS
STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC

E27

DIQLTQSPSS LSASVGDRVT ITCRASKPVD GEGDSYLNWY QQKPGKAPKL LIYAASYLES
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSHEDPY TFGQGTKVEI KRTVAAPSVF
IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS
STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC

HEAVY CHAIN

E26

EVQLVESGGG LVQPGGSLRL SCAVSGYSIT SGYSWNWIRQ APGKGLEWVA SITYDGSTNY
NPSVKGRITI SRDDSKNTFY LQMNSLRAED TAVYYCARGS HYFGHWHFAV WGQGTLVTVS
SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS
SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP SNTKVDKKVE PKSCDKTHT

E27

EVQLVESGGG LVQPGGSLRL SCAVSGYSIT SGYSWNWIRQ APGKGLEWVA SIKYSGETKY
NPSVKGRITI SRDDSKNTFY LQMNSLRAED TAVYYCARGS HYFGHWHFAV WGQGTLVTVS
SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS
SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP SNTKVDKKVE PKSCDKTHT

FIG._13

E26

EVQLVESGGG LVQPGGSLRL SCAVSGYSIT SGYSWNWIRQ APGKGLEWVA SITYDGSTNY
NPSVKGRITI SRDDSKNTFY LQMNSLRAED TAVYYCARGS HYFGHWHFAV WGQGTLVTVS
SEGGGSEGGG SEGGGSDIQL TQSPSSLSAS VGDRVTITCR ASKPVDGEGD SYLNWYQQKP
GKAPKLLIYA ASYLESGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SHEDPYTFGQ
GTKVEIKR

E27

EVQLVESGGG LVQPGGSLRL SCAVSGYSIT SGYSWNWIRQ APGKGLEWVA SIKYSGETKY
NPSVKGRITI SRDDSKNTFY LQMNSLRAED TAVYYCARGS HYFGHWHFAV WGQGTLVTVS
SEGGGSEGGG SEGGGSDIQL TQSPSSLSAS VGDRVTITCR ASKPVDGEGD SYLNWYQQKP
GKAPKLLIYA ASYLESGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SHEDPYTFGQ
GTKVEIKR

FIG._14

LIGHT CHAIN

E26

DIQLTQSPSS LSASVGDRVT ITCRASKPVD GEGDSYLNWY QQKPGKAPKL LIYAASYLES
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSHEDPY TFGQGTKVEI KRTVAAPSVF
IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS
STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC

E27

DIQLTQSPSS LSASVGDRVT ITCRASKPVD GEGDSYLNWY QQKPGKAPKL LIYAASYLES
GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSHEDPY TFGQGTKVEI KRTVAAPSVF
IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS
STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC

HEAVY CHAIN

E26

EVQLVESGGG LVQPGGSLRL SCAVSGYSIT SGYSWNWIRQ APGKGLEWVA SITYDGSTNY
NPSVKGRITI SRDDSKNTFY LQMNSLRAED TAVYYCARGS HYFGHWHFAV WGQGTLVTVS
SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS
SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPC

E27

EVQLVESGGG LVQPGGSLRL SCAVSGYSIT SGYSWNWIRQ APGKGLEWVA SIKYSGETKY
NPSVKGRITI SRDDSKNTFY LQMNSLRAED TAVYYCARGS HYFGHWHFAV WGQGTLVTVS
SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS
SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPC

FIG._15